

Sujit Silas Armstrong Suthahar

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RESEARCH EXPERIENCE

UCLA Dermatology and Immunology

Los Angeles, CA

Graduate Student Researcher II

Apr 2025 – present

- Led the atlas-level integration of scRNA-seq datasets with scvi-tools to build a skin atlas to study wound healing in mice
- Modeled RNA velocity data to identify wound healing trajectories and perturbation targets for accelerated recovery
- Fine-tuned the Arc Institute's State Transition and Stack models with using LoRA adapters with RNA velocity guided vectors enabling stable training and improved perturbation prediction accuracy
- Harvested primary murine bone marrow derived macrophages (BMDMs) and conducted controlled stimulation and perturbation experiments, with downstream qPCR and RNA-seq to quantify transcriptional responses

UCLA Institute for Society and Genetics

Los Angeles, CA

Graduate Student Researcher I

Sep 2023 - Mar 2025

- Led multi-omics analysis (RRBS, WGBS, ATAC-seq, RNA-seq) to elucidate epigenetic effects of environmental toxins
- Leveraged PARAFAC AO-ADMM based CMF to uncover shared latent factors across biological modalities
- Developed a genome-wide differentially methylated region (DMR) annotation pipeline integrating chromatin state and ENSEMBL annotations
- Designed Nextflow pipelines for reproducible bioinformatics workflows on distributed compute

UCLA Biomedical AI Research Lab

Los Angeles, CA

Researcher

Sep 2023 - Jun 2024

- Designed a multiple instance learning classifier for thyroid nodule classification achieving 11% sensitivity improvement
- Developed U-Net based segmentation model with enhanced skip connections for biopsy needle segmentation
- Applied transfer learning with pre-trained VGG-16 backbone to extract features from ultrasound and CT images, enabling efficient model training on limited medical imaging data

WORK EXPERIENCE

Arkim Inc x Databricks

Los Angeles, CA

Data Engineer (Co-op)

Apr 2025 - Oct 2025

- Developed an agentic RAG system with LangGraph for engineering document retrieval and knowledge extraction task
- Built an in-house MCP server for agentic access to DynamoDB and worked on other software development tickets
- Created a model-serving endpoint on Databricks with OAuth to run a multimodal document processing pipeline on serverless compute, achieving low-latency inference (2-3s per document) across 1,000+ engineering documents
- Leveraged open source multimodal embedding models by hosting on Databricks to perform image retrieval tasks with cross-functional team collaboration

GRAIL

Menlo Park, CA

Computational Biology & Machine Learning Research Intern

Jun 2024 - Sep 2024

- Optimized feature selection for argmax classifier improving cfDNA probe specificity for 150+ probes on the Galleri targeted assay panel
- Designed a genome annotation toolkit for DMRs, deployed internally and re-annotated 400+ datasets
- Refactored analytical functions and merged pull requests to internal codebase

La Jolla Institute for Immunology

La Jolla, CA

Bioinformatics Specialist

Jun 2021 - Jul 2023

- Led RNA-seq, scRNA-seq, CITE-seq, and TCR-seq analyses using DESeq2, edgeR, Scanpy, Seurat, and ad hoc pipelines
- Designed statistical models for analyzing 348,000+ TCR sequences, identifying 672 APOB-reactive T-cell clones and 532 conserved CDR3 motifs to track disease-specific clonotypes across donors
- Developed a computational toolkit for optimizing antibody titration for 124 antibodies in CITE-seq
- Automated sequencing data alignment and analysis pipelines reducing processing time by 30%

TECHNICAL SKILLS

Programming: Python, R, TypeScript, Bash/Shell, SQL, C/C++, LaTeX

ML/DL: PyTorch, Scikit-learn, TensorFlow, Keras, LangChain, LangGraph, Transformers, Hugging Face

Cloud & Infra: AWS (EC2, Lambda, S3, DynamoDB), Docker, Git, CI/CD, MLOps, Databricks

Data Analytics: Pandas, NumPy, Apache Spark, ETL Pipelines, Matplotlib, Seaborn, Plotly

Wet Lab: Primary immune cell culture (macrophages, BMDMs), stimulation and activation-induced marker assays, RNA extraction, cDNA synthesis, qPCR, RNA-seq library preparation

Bioinformatics: DESeq2, Seurat, Scanpy, Nextflow, Cell Ranger, Bioconductor, WGCNA, MiXCR, edgeR

PUBLICATIONS

Peer-Reviewed Journal Articles (First Author / Co-First)

- **Suthahar SSA**, Roy P, Makings J and Ley K (2024) Identification of apolipoprotein B–reactive CDR3 motifs allows tracking of atherosclerosis-related memory CD4+T cells in multiple donors. *Front. Immunol.* 15:1302031. doi:10.3389/fimmu.2024.1302031.
- **Armstrong, SS**, Chen, DG, Kumar, S, et al. (2025). CITE-Seq Analysis Reveals a Differential Natural Killer Cell SPON2 Expression in Cardiovascular Disease Patients. *International Journal of Molecular Sciences*, 26(3), 1369.
- **Armstrong Suthahar, SS**, Nettersheim, FS, Alimadadi, A, et al. (2024). Olfr2-positive macrophages originate from monocytes proliferate in situ and present a pro-inflammatory foamy-like phenotype. *Cardiovascular Research*, 120(13), 1577-1589.

Preprints (First Author)

- **Suthahar, SSA**, Allard, P. (2025). Integrative Analysis of Epigenetic, Transcriptomic, and Metabolomic Responses to Arsenic Exposure Using CMF. arXiv:2510.19294. [Submitted]
- **Armstrong, SS**, Ruan, D. (2025). Generation of synthetic scRNA-seq-like transcriptomes using a GAN from RNA-seq data. bioRxiv.

Selected Co-Authored Publications

- Yuko Tada, **Armstrong, SS**, et al. Proinflammatory and cytotoxic CD38+HLA-DR+ effector memory CD8+ T cells are peripherally expanded in human cardiac allograft vasculopathy, *American Journal of Transplantation*, 2025.
- Roy, P, Bellapu, A, **Suthahar, SSA**, et al. (2025). Loss of effector Treg signature in APOB-reactive CD4+ T cells in CAD. *Nature Cardiovascular Research*, 1-16.
- Nettersheim, FS, Brunel, S, Sinkovits, RS, **Armstrong, SS**, et al. (2025). PD-1 and CD73 on naive CD4+ T cells synergistically limit responses to self. *Nature Immunology*, 26(1), 105-115.
- Athreya, S, Melehy, A, **Suthahar, SSA**, et al. (2025). Combining Ultrasound Imaging and Molecular Testing in a Multimodal DL Model for Thyroid Nodules. *Thyroid*, 35(5), 590-594.
- Oliaeimotlagh, M, Kumar, S, Taraskin, A, **Suthahar, SSA**, et al. (2025). Automated denoising of CITE-seq data with ThresholdR. *Cell Reports Methods*, 5(7).
- Freuchet, A, Roy, P, **Armstrong, SS**, et al. (2023). Identification of human exTreg cells as CD16+ CD56+ cytotoxic CD4+ T cells. *Nature Immunology*, 24(10), 1748-1761.
- Nettersheim, FS, **Armstrong, SS**, Durant, C, et al. (2022). Titration of 124 antibodies using CITE-Seq on human PBMCs. *Scientific Reports*, 12(1), 20817.

* Please check my [Google Scholar](#) page for information on additional publications

Poster Presentations & Published Abstracts (Most Recent)

- **Armstrong Suthahar, SS**, Allard, P. “Integrative Multi-Omics Analysis of Arsenic Toxicity Using CMF.” Society of Toxicology (SOT) March 2025, Orlando, FL.
- Shreeram Athreya, Andrew Melehey, **Armstrong Suthahar, SS**, “Multi-Modal Deep Learning for Thyroid Nodule Risk Stratification.” UCLA JCCC Symposium, Mar 2024.
- **Armstrong Suthahar, SS**. “Generation of synthetic scRNA-seq-like transcriptomes using a GAN from RNA-seq data.” UCLA Bioengineering Conference, Feb 2024.

SELECT PROJECTS

- Coupled Matrix Factorization for Multi-Omics Integration 2025
- Developed CMF framework to jointly decompose multi-omics data (methylation, transcriptomic, metabolomic) identifying shared latent factors; published in arXiv
- Finetuning Mistral-7B-Instruct 2025
- Finetuned Mistral-7B-Instruct-v0.3 with LoRA using the official mistral-finetune framework to build a domain-adapted model for technical question answering
- State Model Experimentation 2025
- Experimented with Arc Institute’s State Embedding (SE) and State Transition (ST) model. Worked on conditioning these models on time-course data, capturing temporal patterns and modeling effects in skin wound scRNA-seq experiments
- Neural Sequence Decoder 2025
- Adapted a five-layer unidirectional GRU and conducted a four-model ablation study to evaluate data augmentation and training strategies for neural speech decoding, based on results from the 2024 BCI competition

ACADEMIC SERVICE AND LEADERSHIP

UCLA Samueli School of Engineering

Graduate Student Representative, Faculty Executive Committee (FEC)

- Led school-wide survey of 200+ students; identified 70% of master’s students require a course in research methodology, informing curriculum policy changes
- Facilitated computational workshops bridging wet lab-dry lab divide and provided academic consulting to international students; recognized with Engineering Achievement Award (2025)

Los Angeles, CA

Jan 2024 - Dec 2024

Regulatory Consultant*Stealth Startup (UCLA Licensed Technology)***Los Angeles, CA***Sep 2024 - present*

- Provided FDA 510(k) clearance analysis and evaluation for electrical stimulation / TENS wound care device, identifying predicate devices and product codes for submission
- Analyzed reimbursement landscape and identified optimal billing codes to maximize insurance coverage for medical device commercialization

RELEVANT COURSEWORK

ECE C247 - Neural Networks and Deep Learning, ECE C239AS - Signals and Systems: Advanced Neural Networks and Deep Learning, BIOMATH 201- Deterministic Models in Biology, PBMED 209 - Signal and Image Processing, BIOE 275 - Machine Learning and Data Driven Modeling, BIOE 224B - Advanced Imaging Informatics, GEN 242 - Data Analysis in Genome Biology, ECE C243A – Brain Computer Interfaces, BIOL 119 - Introduction to Genomics and Bioinformatics, BIOL 115 - Human Genetics, AAI Courses in Immunology 2025

AWARDS AND HONORS

- Engineering Achievement Award for Student Welfare, UCLA Jun 2025
- UCR Highlander Union Excellence Award, UC Riverside Education Mar 2019

EDUCATION

University of California-Los Angeles*Ph.D. in Bioengineering*

GPA: 4.00/4.00

Los Angeles, CA*Apr 2025 - present***University of California-Los Angeles***M.S. in Bioengineering*

GPA: 3.98/4.00

Los Angeles, CA*Sep 2023 - Mar 2025***University of California-Riverside***Bachelor of Science, Biology (Honors)*

GPA: 3.60/4.00

Riverside, CA*Sep 2017 - Mar 2021*